

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/381,750

Source: 1Fw/6

Date Processed by STIC: 8/23/05

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/381,750

DATE: 08/23/2005

TIME: 13:58:23

Input Set : E:\ARCD333.APP.txt

Output Set: N:\CRF4\08232005\I381750.raw

3 <110> APPLICANT: PARMACEK, MICHAEL S.  
 4 SOLWAY, JULIAN  
 6 <120> TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION  
 8 <130> FILE REFERENCE: ARCD:333-1  
 10 <140> CURRENT APPLICATION NUMBER: 09/381,750  
 C--> 11 <141> CURRENT FILING DATE: 2001-01-25  
 13 <150> PRIOR APPLICATION NUMBER: PCT/US97/16204  
 14 <151> PRIOR FILING DATE: 1997-08-29  
 16 <150> PRIOR APPLICATION NUMBER: 09/380,928  
 17 <151> PRIOR FILING DATE: 1999-09-09  
 19 <150> PRIOR APPLICATION NUMBER: 08/726,807  
 20 <151> PRIOR FILING DATE: 1996-10-07  
 22 <150> PRIOR APPLICATION NUMBER: 60/004,868  
 23 <151> PRIOR FILING DATE: 1995-10-05  
 25 <160> NUMBER OF SEQ ID NOS: 51  
 27 <170> SOFTWARE: PatentIn Ver. 2.1  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 1419  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Artificial Sequence  
 34 <220> FEATURE:  
 35 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 36 Primer  
 38 <400> SEQUENCE: 1  
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 40 tgacccttcc ttcagatgcc acaaggagggt gctggaggttc tatgcaccaa tagcttaaac 120  
 41 cagccagggt ggctgtagtg gattgagcgt ctgaggctgc acctctctgg cctgcagcca 180  
 42 gttctgggtg agactgaccc tgccctgaggg ttctctcctt ccctctctct actcctttct 240  
 43 ccctctccct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga 300  
 44 gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca 360  
 45 cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac 420  
 46 tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg 480  
 47 tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt 540  
 48 aggatctttc acgataagga ctattttgaa gggaggaggagg gtgacactgt cctagtcctc 600  
 49 ttaccctagt gtctccagcc ttgccaggcc ttaaacatcc gccattgtc accgctctag 660  
 50 aaggggccag ggttgacttg ctgctaaaca aggcactccc tagagaagca cccgctagaa 720  
 51 gcataccata cctgtgggca ggatgaccca tgttctgcc cgcacttggt agccttgga 780  
 52 aggccacttt gaacctcaat tttctcaact gttaaatggg gtggttaactg ctatctcata 840  
 53 ataaaggggg acgtgaaagg aaggcgtttg catagtgcct ggttgtagcag ccaggctgca 900  
 54 gtcaagacta gttcccacca actcgatttt aaagccttgc aagaaggtgg cttgtttgtc 960  
 55 ccttgtaggt tcctttgtcg ggccaaactc tagaatgcct ccccttttct ttctcattga 1020  
 56 agagcagacc caagtccggg taacaaggaa gggtttcagg gtccctgcca taaaaggttt 1080  
 57 ttcccgccg ccctcagcac cgccccgccc cgacccccgc agcatctcca aagcatgcag 1140

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58 agaatgtctc cggtgcccc cgacagactg ctccaacttg gtgtctttcc ccaaatatgg 1200
59 agcctgtgtg gagtgagtgg ggcggcccg ggtggtgagc caagcagact tccatgggca 1260
60 gggaggggcg ccagcggacg gcagaggggt gacatcactg cctaggcggc ctttaaacc 1320
61 ctacaccagc cggcgcccca gccgtctgc ccagcccag acaccgaagc tactctcctt 1380
62 ccagtccaca aacgaccaag ccttgtaagt gcaagtcac 1419
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66 <211> LENGTH: 991
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
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72 <222> LOCATION: (38)..(217)
74 <220> FEATURE:
75 <221> NAME/KEY: CDS
76 <222> LOCATION: (322)..(447)
78 <220> FEATURE:
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80 <222> LOCATION: (866)..(967)
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
84 Primer
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88 Met Ala Asn Lys Gly Pro
89 1 5
91 tcc tac ggc atg agc cga gaa gtg cag tcc aaa att gag aag aag tat 103
92 Ser Tyr Gly Met Ser Arg Glu Val Gln Ser Lys Ile Glu Lys Lys Tyr
93 10 15 20
95 gac gag gag ctg gag gag cga cta gtg gag tgg att gta gtg cag tgt 151
96 Asp Glu Glu Leu Glu Glu Arg Leu Val Glu Trp Ile Val Val Gln Cys
97 25 30 35
99 ggc cct gat gta ggc cgc cca gat cgt ggg cgc ctg ggc ttc cag gtg 199
100 Gly Pro Asp Val Gly Arg Pro Asp Arg Gly Arg Leu Gly Phe Gln Val
101 40 45 50
103 tgg ctg aag aat ggt gtg gtgagtaacc cttgcgaagg gaatctaggg 247
104 Trp Leu Lys Asn Gly Val
105 55 60
107 atgtgtatgc cgccctacaa actgtgagac agactccctg agctgagtgt tcagtttgtt 307
109 tctgtacctg gcag att ctg agc aaa ttg gtg aac agc ctg tat cct gag 357
110 Ile Leu Ser Lys Leu Val Asn Ser Leu Tyr Pro Glu
111 65 70
113 gga tcg aag cca gtg aag gtg cct gag aac cca ccc tcc atg gtc ttt 405
114 Gly Ser Lys Pro Val Lys Val Pro Glu Asn Pro Pro Ser Met Val Phe
115 75 80 85
117 aag cag atg gaa cag gtg gct caa ttc ttg aag gca gct gaa 447
118 Lys Gln Met Glu Gln Val Ala Gln Phe Leu Lys Ala Ala Glu
119 90 95 100
121 gattatggag tcatcaagac tgacatgttc cagactgttg acctctatga aggtataagg 507
123 aaaaaagggc tggagccagt gggcgagtgg agagcaagat tatcagtcaa ggagaaggaa 567

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125 tatcaaaagc cacaaccagc tctgttgatg tgttcatagc aggaatggga tatgccaaga 627
127 gaacacatag caaggggacc agcttggtgg tacagcattt ccttctgggt acaagggcct 687
129 gttttggatc ctagaatatac aaatatatac cacaccatac tcactagggt ttagaatatg 747
131 gtctcttgaa cctcttgat ttggtgccac ttgctccttg gttggaccat ttttgaagct 807
133 gggcaggtat tgctatatatg gtctgaaat tagctccctg gccactcttc tcataggt 865
135 aag gat atg gca gca gtg cag agg act cta atg gct ttg ggc agt ttg 913
136 Lys Asp Met Ala Ala Val Gln Arg Thr Leu Met Ala Leu Gly Ser Leu
137      105      110      115
139 gct gtg acc aaa aac gat gga aac tac cgt gga gat ccc aac tgg ttt 961
140 Ala Val Thr Lys Asn Asp Gly Asn Tyr Arg Gly Asp Pro Asn Trp Phe
141      120      125      130
143 atg aag tatgtgtcca ctgggtctct ctgt 991
144 Met Lys
145 135
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149 <211> LENGTH: 60
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
155 Peptide
157 <400> SEQUENCE: 3
158 Met Ala Asn Lys Gly Pro Ser Tyr Gly Met Ser Arg Glu Val Gln Ser
159 1 5 10 15
160 Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Glu Arg Leu Val Glu
161 20 25 30
162 Trp Ile Val Val Gln Cys Gly Pro Asp Val Gly Arg Pro Asp Arg Gly
163 35 40 45
164 Arg Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val
165 50 55 60
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 42
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
175 Peptide
177 <400> SEQUENCE: 4
178 Ile Leu Ser Lys Leu Val Asn Ser Leu Tyr Pro Glu Gly Ser Lys Pro
179 1 5 10 15
180 Val Lys Val Pro Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu
181 20 25 30
182 Gln Val Ala Gln Phe Leu Lys Ala Ala Glu
183 35 40
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 34
188 <212> TYPE: PRT
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:

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192 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
193     Peptide
195 <400> SEQUENCE: 5
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199           20           25           30
200 Met Lys
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205 <211> LENGTH: 575
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
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210 <221> NAME/KEY: CDS
211 <222> LOCATION: (28)..(168)
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
215     Primer
217 <400> SEQUENCE: 6
218 acttaccctg gttccttttc ttctagg aaa gcc cag gag cat aag agg gac ttc 54
219                               Lys Ala Gln Glu His Lys Arg Asp Phe
220                               1           5
222 aca gac agc caa ctg cag gag ggg aag cac gtc att ggc ctt caa atg 102
223 Thr Asp Ser Gln Leu Gln Glu Gly Lys His Val Ile Gly Leu Gln Met
224 10           15           20           25
226 ggc agc aac aga gga gcc tcg cag gct ggc atg aca ggc tat ggg cga 150
227 Gly Ser Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr Gly Arg
228           30           35           40
230 ccc cgg cag atc atc agt tagaaaggga aggccagccc tgagctgcag 198
231 Pro Arg Gln Ile Ile Ser
232           45
234 catcctgctt agcctgcctc acaaatgcct atgtaggttc ttagccctga cagctctgag 258
236 gtgtcactgg gcaaagatga ctgcacatgg gcagctccca cctatcctta gcctcagccc 318
238 agcatcttac ccagagcca ccaactgcct ggcccctgtt ccagctgta cccccacctc 378
240 tactgttcct ctatccttg agtaagcagg gagaagtggg ctggggtagc tggctgtagg 438
242 ccagcccact gtccttgata tcgaatgtcc tttgaaggag acccagccca gcctctacat 498
244 cttttcctgg aatatgtttt tgggttgaaa ttcaaaaagg aaaaaagaaa aatatataaa 558
246 tatatatata tatatac 575
249 <210> SEQ ID NO: 7
250 <211> LENGTH: 47
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
256     Peptide
258 <400> SEQUENCE: 7
259 Lys Ala Gln Glu His Lys Arg Asp Phe Thr Asp Ser Gln Leu Gln Glu
260   1           5           10           15
262 Gly Lys His Val Ile Gly Leu Gln Met Gly Ser Asn Arg Gly Ala Ser

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263          20          25          30
265 Gln Ala Gly Met Thr Gly Tyr Gly Arg Pro Arg Gln Ile Ile Ser
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272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <221> NAME/KEY: CDS
277 <222> LOCATION: (77)..(679)
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
281     Primer
283 <400> SEQUENCE: 8
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286 ccttctctgc ctcaac atg gcc aac aag ggt cca tcc tac ggc atg agc cga 112
287             Met Ala Asn Lys Gly Pro Ser Tyr Gly Met Ser Arg
288             1             5             10
290 gaa gtg cag tcc aaa att gag aag aag tat gac gag gag ctg gag gag 160
291 Glu Val Gln Ser Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Glu
292             15             20             25
294 cga cta gtg gag tgg att gta gtg cag tgt ggc cct gat gta ggc cgc 208
295 Arg Leu Val Glu Trp Ile Val Gln Cys Gly Pro Asp Val Gly Arg
296             30             35             40
298 cca gat cgt ggg cgc ctg ggc ttc cag gtg tgg ctg aag aat ggt gtg 256
299 Pro Asp Arg Gly Arg Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val
300             45             50             55             60
302 att ctg agc aaa ttg gtg aac agc ctg tat cct gag gga tcg aag cca 304
303 Ile Leu Ser Lys Leu Val Asn Ser Leu Tyr Pro Glu Gly Ser Lys Pro
304             65             70             75
306 gtg aag gtg cct gag aac cca ccc tcc atg gtc ttt aag cag atg gaa 352
307 Val Lys Val Pro Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu
308             80             85             90
310 cag gtg gct caa ttc ttg aag gca gct gaa gat tat gga gtc atc aag 400
311 Gln Val Ala Gln Phe Leu Lys Ala Ala Glu Asp Tyr Gly Val Ile Lys
312             95             100             105
314 act gac atg ttc cag act gtt gac ctc tat gaa ggt aag gat atg gca 448
315 Thr Asp Met Phe Gln Thr Val Asp Leu Tyr Glu Gly Lys Asp Met Ala
316             110             115             120
318 gca gtg cag agg act cta atg gct ttg ggc agt ttg gct gtg acc aaa 496
319 Ala Val Gln Arg Thr Leu Met Ala Leu Gly Ser Leu Ala Val Thr Lys
320             125             130             135             140
322 aac gat gga aac tac cgt gga gat ccc aac tgg ttt atg aag aaa gcc 544
323 Asn Asp Gly Asn Tyr Arg Gly Asp Pro Asn Trp Phe Met Lys Lys Ala
324             145             150             155
326 cag gag cat aag agg gac ttc aca gac agc caa ctg cag gag ggg aag 592
327 Gln Glu His Lys Arg Asp Phe Thr Asp Ser Gln Leu Gln Glu Gly Lys
328             160             165             170
330 cac gtc att ggc ctt caa atg ggc agc aac aga gga gcc tcg cag gct 640

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/381,750

DATE: 08/23/2005

TIME: 13:58:24

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date